

Integrative Cancer Research Special Interest Group Teleconference

Microarray Repository SIG Meeting Minutes

Date, Time & Location:	September 1, 2004, 2004 2:00 – 3:00 EDT		
Attendees:	Don	Baldwin	Penn
	Terry	Braun	University of Iowa
	Robert	Clarke	Lombardi Cancer Center
	Joel	Dubbels	IBM
	Steve	Enkemann	University of South Florida
	Mervi	Heiskanen	NCI
	Chris	Kingsley	UC San Francisco
	Juli	Klemm	Booz Allen Hamilton
	Steve	Marron	University of North Carolina
	John	Osborn	Northwestern University
	John	Powell	NCI
	Michael	Showe	Wistar
	Michael	Nebozhyn	Wistar
	Wen-Hwai	Horng	Wistar
	Walter	Mankowski	Wistar
	Louise	Showe	Wistar
	Taku	Tokuyasu	UC San Francisco
	Naveen	Vinukonda	Institute For Cancer Prevention
	Edith	Zang	Institute For Cancer Prevention
	Claire	Zhu	Booz Allen Hamilton
	Julie	Zhu	Northwestern University
Introduction:	<u>Roll-call, open meeting, review meeting goals</u> <ul style="list-style-type: none">- Review of last meeting- Update on caArray- Review of face-to-face meeting- Set agenda for next meeting		
Review Discussions	<u>Review discussion of last meeting</u> <ul style="list-style-type: none">- Last month's meeting was focused on data exchange with caArray. Mervi gave an overview of tools that will be available to import/export data to/from caArray. Slides and minutes are available on the forum for those who missed the meeting.<ul style="list-style-type: none">o Review uploading microarray expression values to caArray (Mervi)<ul style="list-style-type: none">▪ The MAGE-ML created by caArray has an expression value associated with it, but it is not in the native format. One can submit expression value in MAGE-ML format, but will not be able to get original file back out from caArray.▪ Does caArray incorporate MAGE-OM? (Julie Zhu)		



Integrative Cancer Research Special Interest Group Teleconference

- Yes, caArray is designed on MAGE 1.1.
- How similar is caArray compared to MIAME Express? (Julie Zhu)
 - Very different, but captures the same information. If you have used MIAME Express to generate MAGE-ML, you will be able to use the information for caArray.
- MIAME Express does not accept image files. Does caArray has features for importing image data file?
 - We don't have image file in the database. What you can do is to attach the image files to the experiment.

Update on caArray release and user acceptance testing

- Mervi gave an update on caArray user acceptance testing.
 - The user acceptance testing has been delayed to allow developers more time to fix the bugs, and give more time to the cancer centers to provide feedback.
 - Test is schedule for 9/21/04, for about 2 weeks.
 - Version 1.0 on 9/23/04 Version 1.1 planning meeting schedule for 10/5/04.

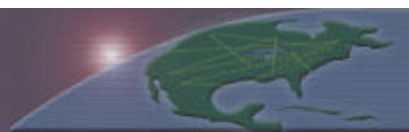
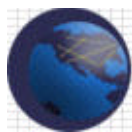
Review discussion of face-to-face meeting

- Update on the issue of loading caArray MAGE-OM to caDSR.
 - The MAGE-OM object is included in caArray but note that it has caArray-specific restrictions.
 - Originally had thought of implementing two object models: MAGE-OM and caArray. But it was not possible to reference from caArray to MAGE through caDSR.
 - Only caArray definitions are included in CDE, no values yet. Also note that the MAGE ontology is currently in the private EVS. Once it is moved to the public server, we should be able to reference that from caDSR.
 - caArray currently gets MAGE ontology directly from EVS, not through caDSR.
 - How easy is it to implement caArray if you are using another database such as EBI, which was implemented exactly as a MAGE-OM?
 - This is more of a developer's question. Design documents are available in the CaArray developer's documentation on the web site. You can also email your technical questions to Juli.
- Follow up on the use cases request from the Architecture group.
 - Goal is to facilitate and support the Architecture group to identify architectural issues they need to be working on.
 - Juli has emailed a use case example written by Patrick McConnell of Duke. In this example, both near term and long term usage of the proteomics data are presented. Each cancer center should submit a similar use case.
 - Timeframe for submission is 9/17/04, approximately 2 weeks from



Integrative Cancer Research Special Interest Group Teleconference

- today.
- From whose perspective should the use cases be written? (Terry Braun)
 - Ideally, the use case should reflect a combination of both developer' and end user' points of views.
 - Are the use cases from the perspectives of issues want to be raised with the Architecture group? Are they a subset of the use cases people put together in SOWs? (Terry Braun)
 - These are use cases with different end goal, which is to help architecture group with the platforms and technologies issues.
 - For microarray data, these would be caArray use cases? (Julie Zhu)
 - Yes, i.e. how you want caArray to interact with analytic tools and data.
 - Follow up on request from face-to-face meeting regarding access to crossing-cutting workspaces. Juli has been talking with the cross-cutting workspace leads on this issue.
 - One model is to have a go-to person from the cross-cutting workspaces to be assigned to each SIG. Juli asked the group for comments/feedback.
 - Steve Marron wondered if this model would be the right level of granularity, whether one person would be able to handle to work load. He suggested that the point person be assigned to projects, rather than to the whole SIG.
 - It may be un-realistic to have a point person assigned to each projects, given the large number of projects in ICR. The solution would be to limit the number of projects assigned to one person. For certain SIGs, maybe the number of projects requires more than one person.
 - It also depends on the manpower of the cross-cutting workspaces (Steve)
 - Another issue raised at the face-to-face meeting was the need for coordination across projects within the SIG.
 - Juli proposed to assign a point person for each SIG. However, this may not be necessary for the microarray SIG, as most of the projects are centered around data exchange with caArray. Juli asked feedback from the group.
 - What would the point person have to do? (Steve)
 - For example, within the Pathways SIG, there are three projects, and it is necessary to come up and agree upon a common way of representing the pathway data. For the Microarray SIG, the need for coordination is not as pressing, because data exchange format already exists.
 - There was a big discussion at the face-to-face meeting on gene names. How does it interface with MAGE-ML? (Steve)
 - Initial thought was that genome annotation SIG would be charged with resolving that issue, but clearly it is relevant to the microarray SIG as well. One needs to understand how



Integrative Cancer Research Special Interest Group Teleconference

MAGE-ML captures gene annotation. This may be a point of harmonization across ICR.

- The most important thing to identify in microarray is the spots, or probe sets, which are translated to genes by various software. The probe ID is a useful identifier by itself, as opposed to gene/protein name. We need to draw a line between storing information in the database and processing that information. (Steve E)
- What would be the mechanism for the point person to carry out the work? (Steve M)
 - Probably would depend on the person and the topic. Meetings and offline discussions are some examples.
- Instead of setting up an elaborate hierarchy of networks or contacts, which may never be used, it maybe better to leave it until a particular need arises, and then to identify a point person to follow up on it. (Michael Showe)
- This SIG is ahead of many other SIGs because many of the standards and tools already exist. We are in a good position to start thinking about the next generation tools. (Don Baldwin)

Other Items Discussed

Action Items

Name Responsible	Action Item	Date Due	Notes
Juli Klemm	Send John Powell use case example	9/1/04	
Juli Klemm	Distribute meeting minutes	9/14/04	